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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/825,776	04/16/2004	Robert C. Getts	4081.010.200	8737

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EXAMINER	
STRZELECKA, TERESA E	
ART UNIT	PAPER NUMBER
1637	

DATE MAILED: 12/11/2006

Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary	Application No.	Applicant(s)	
	10/825,776	GETTS ET AL.	
	Examiner	Art Unit	
	Teresa E. Strzelecka	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *25 September 2006*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-24* is/are pending in the application.

4a) Of the above claim(s) *9-24* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1-8* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☒ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☒ Other: *Notice to Comply*.

DETAILED ACTION

Election/Restrictions

1. Applicant's election without traverse of Species A and E in the reply filed on September 25, 2006 is acknowledged.

2. Claims 9-24 are withdrawn from further consideration pursuant to 37 CFR 1.142(b) as being drawn to a nonelected species, there being no allowable generic or linking claim. Election was made **without** traverse in the reply filed on September 25, 2006.

3. Claims 1-8 will be examined.

Sequence Rules Compliance

4. This application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 C.F.R. §§ 1.821-1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequence And/Or Amino Acid Sequence Disclosures. Applicant must comply with the requirements of the sequence rules (37 CFR 1.821 - 1.825) before the application can be examined under 35 U.S.C. §§ 131 and 132.

APPLICANT IS GIVEN time of response to this office action WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821-1.825. Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Pages 47, 48 and 50 of the specification contain sequences without SEQ ID NOs. If these sequences are already present in the previously submitted sequence listing, specification needs to be amended to include SEQ ID NOs. If these sequences were not included in the sequence listing, a new sequence listing containing them needs to be submitted.

Claim Rejections - 35 USC § 102

5. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.
>
> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.

6. Claims 1-5 are rejected under 35 U.S.C. 102(a) as being anticipated by Stears et al. (Physiol. Genomics, vol. 3, pp. 93-99, August 2000).

Regarding claim 1, Stears et al. teach a method for determining the presence of at least one specific nucleotide sequence in a target nucleic acid reagent extracted from a biological sample, said method comprising the steps of:

(a) concurrently contacting a microarray with:

(i) a target nucleic acid reagent, said target nucleic acid reagent having a nucleotide sequence, said nucleotide sequence further including a capture sequence (Fig. 1; page 93, third paragraph; page 95, last paragraph), and

(ii) a capture reagent, said capture reagent having at least one first arm having a label capable of emitting a detectable signal and at least one second arm having a nucleotide

sequence complementary to said capture sequence of said target nucleic acid reagent (Fig. 1; page 94, last paragraph; page 95; page 97, first paragraph);

said microarray having thereon a plurality of features, each of said plurality of features including a probe nucleotide sequence (page 93, fourth paragraph; page 94, first paragraph); and

(b) treating the microarray from step (a) at a temperature and for a time sufficient to induce said nucleotide sequence of said target nucleic acid to hybridize to the probe nucleotide sequence complementary thereto on the microarray, and to induce said capture reagent to hybridize to said capture sequence of said nucleotide sequence of said target nucleic acid hybridized to the microarray (page 93, third paragraph; page 94, last paragraph; page 95, first paragraph).

Regarding claim 2, Stears et al. teach detection of patterns generated by hybridized probes (Fig. 1).

Regarding claims 3 and 5, Stears et al. teach dendrimers (page 95, paragraphs 2-4).

Regarding claim 4, Stears et al. teach cDNA capture reagent (page 93, third paragraph).

7. Claims 1-5 are rejected under 35 U.S.C. 102(e) as being anticipated by Goldberg et al. (U.S. Patent No. 6,203,989 B1), as evidenced by Lockhart et al. (Nature Biotechnol., vol. 14, pp. 1675-1680, 1996).

Regarding claim 1, Goldberg et al. teach a method for determining the presence of at least one specific nucleotide sequence in a target nucleic acid reagent extracted from a biological sample, said method comprising the steps of:

(a) concurrently contacting a microarray with:

(i) a target nucleic acid reagent, said target nucleic acid reagent having a nucleotide sequence, said nucleotide sequence further including a capture sequence (col. 2, lines 9-22; col. 3, lines 45-66), and

(ii) a capture reagent, said capture reagent having at least one first arm having a label capable of emitting a detectable signal and at least one second arm having a nucleotide sequence complementary to said capture sequence of said target nucleic acid reagent (col. 2, lines 43-67; col. 3, lines1-6; col. 7, lines 4-46);

said microarray having thereon a plurality of features, each of said plurality of features including a probe nucleotide sequence (col. 3, lines 45-50); and

(b) treating the microarray from step (a) at a temperature and for a time sufficient to induce said nucleotide sequence of said target nucleic acid to hybridize to the probe nucleotide sequence complementary thereto on the microarray, and to induce said capture reagent to hybridize to said capture sequence of said nucleotide sequence of said target nucleic acid hybridized to the microarray (col. 4, lines 1-4; col. 8, lines 61-67; col. 9, lines 1-12 and 66, 67; col. 10, lines 1-39).

Regarding claim 2, Goldberg et al. teach detecting of a hybridization pattern (col. 10, lines 31-39; col. 15, lines 66, 67; col. 16, lines 1-17).

Regarding claims 3 and 5, Goldberg et al. teach dendrimers (col. 6, lines 19-67; col. 7, lines 1-46).

Regarding claim 4, Goldberg et al. do not specifically teach cDNA targets. However, they teach using high-density arrays of Lockhart et al. for gene expression screening (col. 16, lines 58-63). Lockhart et al. teach cDNA targets (page 1676, fourth paragraph). Therefore, by teaching Lockhart et al. Goldberg et al. inherently teach cDNA targets.

Claim Rejections - 35 USC § 103

8. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the

> subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

9. Claims 6-8 are rejected under 35 U.S.C. 103(a) as being unpatentable over Stears et al. (Physiol. Genomics, vol. 3, pp. 93-99, August 2000) and Urdea et al. (U. S. Patent No. 5,681,697 A).

A) Regarding claims 6-8, Stears et al. teach hybridization at a single temperature, but do not teach two temperatures.

B) Urdea et al. teach an assay in which a capture probe is contacted with a target nucleic acid, which in turn is contacted with a detection probe serving as a signal amplification molecule (Fig. 2-4; Fig. 7; col. 2, lines 54-62; col. 6, lines 7-67). They teach performing the assay at two different temperatures, where the first temperature is higher than a second temperature (col. 3, lines 5-20 and 30-46; col. 12, lines 41-67; col. 13, lines 1-26; col. 21, lines 1-25).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used the different hybridization temperatures of Urdea et al. in the method of Stears et al. The motivation to do so, provided by Urdea et al., is that, as stated by Urdea et al. (col. 12, lines 31-40):

"The primary focus of the present method is on eliminating a number of sources of background noise, by maximizing the interaction of capture extender and label extender probes with the target molecule, minimizing the interaction of capture probes and capture extender molecules with the label probes, label extender molecules and amplifiers, increasing the number of probes and/or hybridization steps necessary to give rise to a target-dependent signal, and reducing the likelihood that incorrect moieties will bind to the support-bound capture probes."

10. Claims 6-8 are rejected under 35 U.S.C. 103(a) as being unpatentable over Goldberg et al. (u.S. Patent No. 6,203,989 B1) and Urdea et al. (U. S. Patent No. 5,681,697 A).

A) Regarding claims 6-8, Goldberg et al. teach hybridization at a single temperature, but do not teach two temperatures.

B) Urdea et al. teach an assay in which a capture probe is contacted with a target nucleic acid, which in turn is contacted with a detection probe serving as a signal amplification molecule (Fig. 2-4; Fig. 7; col. 2, lines 54-62; col. 6, lines 7-67). They teach performing the assay at two different temperatures, where the first temperature is higher than a second temperature (col. 3, lines 5-20 and 30-46; col. 12, lines 41-67; col. 13, lines 1-26; col. 21, lines 1-25).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time of the invention to have used the different hybridization temperatures of Urdea et al. in the method of Goldberg et al. The motivation to do so, provided by Urdea et al., is that, as stated by Urdea et al. (col. 12, lines 31-40):

"The primary focus of the present method is on eliminating a number of sources of background noise, by maximizing the interaction of capture extender and label extender probes with the target molecule, minimizing the interaction of capture probes and capture extender molecules with the label probes, label extender molecules and amplifiers, increasing the number of probes and/or hybridization steps necessary to give rise to a target-dependent signal, and reducing the likelihood that incorrect moieties will bind to the support-bound capture probes."

Double Patenting

11. The nonstatutory double patenting rejection is based on a judicially created doctrine grounded in public policy (a policy reflected in the statute) so as to prevent the unjustified or improper timewise extension of the "right to exclude" granted by a patent and to prevent possible harassment by multiple assignees. A nonstatutory obviousness-type double patenting rejection is appropriate where the conflicting claims are not identical, but at least one examined application claim is not patentably distinct from the reference claim(s) because the examined application claim

is either anticipated by, or would have been obvious over, the reference claim(s). See, e.g., *In re Berg*, 140 F.3d 1428, 46 USPQ2d 1226 (Fed. Cir. 1998); *In re Goodman*, 11 F.3d 1046, 29 USPQ2d 2010 (Fed. Cir. 1993); *In re Longi*, 759 F.2d 887, 225 USPQ 645 (Fed. Cir. 1985); *In re Van Ornum*, 686 F.2d 937, 214 USPQ 761 (CCPA 1982); *In re Vogel*, 422 F.2d 438, 164 USPQ 619 (CCPA 1970); and *In re Thorington*, 418 F.2d 528, 163 USPQ 644 (CCPA 1969).

A timely filed terminal disclaimer in compliance with 37 CFR 1.321(c) or 1.321(d) may be used to overcome an actual or provisional rejection based on a nonstatutory double patenting ground provided the conflicting application or patent either is shown to be commonly owned with this application, or claims an invention made as a result of activities undertaken within the scope of a joint research agreement.

Effective January 1, 1994, a registered attorney or agent of record may sign a terminal disclaimer. A terminal disclaimer signed by the assignee must fully comply with 37 CFR 3.73(b).

12. Claims 1 and 3-5 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1 and 18 of copending Application No. 09/802,162. Although the conflicting claims are not identical, they are not patentably distinct from each other because claims 1 and 18 of the 09/802,162 application are species of claims 1 and 3-5 of the instant application.

Specifically, claim 1 of the instant application is drawn to a method for determining the presence of at least one specific nucleotide sequence in a target nucleic acid reagent extracted from a biological sample, said method comprising the steps of:

(a) concurrently contacting a microarray with:

(i) a target nucleic acid reagent, said target nucleic acid reagent having a nucleotide sequence, said nucleotide sequence further including a capture sequence, and

(ii) a capture reagent, said capture reagent having at least one first arm having a label capable of emitting a detectable signal and at least one second arm having a nucleotide sequence complementary to said capture sequence of said target nucleic acid reagent;

said microarray having thereon a plurality of features, each of said plurality of features including a probe nucleotide sequence; and

(b) treating the microarray from step (a) at a temperature and for a time sufficient to induce said nucleotide sequence of said target nucleic acid to hybridize to the probe nucleotide sequence complementary thereto on the microarray, and to induce said capture reagent to hybridize to said capture sequence of said nucleotide sequence of said target nucleic acid hybridized to the microarray.

Claim 1 of the 09/802,162 application is drawn to a method for detection and assay on a microarray, said method comprising the steps of:

1) taking a microarray having thereon a plurality of features each comprising a first particular first nucleotide sequence;

2) taking a first component comprising cDNA reagents having a capture sequence; and taking a second component comprising a dendrimer having at least one first arm comprising a label and at least one second arm having a second nucleotide sequence;

wherein said cDNA reagents comprise a plurality of different nucleotide sequences, and wherein said capture sequence of said cDNA reagent is a common sequence among said cDNA reagents, said common sequence being complementary to said second nucleotide sequence of said dendrimers, said capture sequence being used for binding of said dendrimers to said cDNA reagents, such that said second arm of said dendrimer can bind to any of said cDNA reagents having said capture sequence by hybridization of said second nucleotide sequence of said dendrimer to said capture sequence;

3) mixing said first and second components at a temperature and for a time sufficient to enable said first component to bind to said second component; and

4) incubating this mixture with said microarray to enable the first nucleotide sequence to bind to said first component, wherein such binding results in the generation of a hybridization pattern on the microarray.

Claim 18 of the 09/802,162 application is a re-stated version of claim 1. Therefore, both claims differ from claims 1 and 3-5 by having cDNA as a target reagent and labeled dendrimer as a capture reagent, anticipating claims 1 and 3-5.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

13. Claims 1 and 3, 5 and 6-8 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 1-3, 19, 29, 30 and 32 of copending Application No. 09/908,950. Although the conflicting claims are not identical, they are not patentably distinct from each other because claims 1-3, 19, 20, 21, 29, 30 and 32 of copending Application No. 09/908,950 are species of the instant claims 1 and 3-8.

Specifically, claim 1 of the instant application is drawn to a method for determining the presence of at least one specific nucleotide sequence in a target nucleic acid reagent extracted from a biological sample, said method comprising the steps of:

(a) concurrently contacting a microarray with:

(i) a target nucleic acid reagent, said target nucleic acid reagent having a nucleotide sequence, said nucleotide sequence further including a capture sequence, and

(ii) a capture reagent, said capture reagent having at least one first arm having a label capable of emitting a detectable signal and at least one second arm having a nucleotide sequence complementary to said capture sequence of said target nucleic acid reagent;

said microarray having thereon a plurality of features, each of said plurality of features including a probe nucleotide sequence; and

(b) treating the microarray from step (a) at a temperature and for a time sufficient to induce said nucleotide sequence of said target nucleic acid to hybridize to the probe nucleotide sequence complementary thereto on the microarray, and to induce said capture reagent to hybridize to said capture sequence of said nucleotide sequence of said target nucleic acid hybridized to the microarray.

Claim 1 of the 09/908,950 application is drawn to a method for determining the presence of a specific nucleotide sequence in an RNA reagent of a target sample, said method comprising the steps of:

a) incubating a mixture comprising:

(i) a first component including an RNA reagent extracted from a target sample, said RNA reagent having a target nucleotide sequence and a capture sequence, and

(ii) a second component comprising a capture reagent, said capture reagent comprising, multiple first arms and multiple second arms, said first arms being arms comprising a label capable of emitting a detectable signal, said second arms being arms comprising a nucleotide sequence complementary to the capture sequence of the RNA reagent of the first component,

at a first temperature to induce the capture sequence of the RNA reagent of the first component to bind to the complementary nucleotide sequence of the capture reagent of the second component, and thereby form a pre-hybridized RNA-capture reagent complex comprising the target nucleotide sequence;

b) contacting the pre-hybridized RNA-capture reagent complex with a microarray having thereon a plurality of features each comprising a particular probe nucleotide sequence; and

c) incubating the pre-hybridized RNA-capture reagent complex on the microarray at a second temperature to hybridize the target nucleotide sequence of the pre-hybridized RNA-capture reagent complex to the complememary probe nucleotide sequence contained within the feature, wherein the presence of such hybridization results in a detectable hybridization pattern for subsequent analysis.

Claims 2 and 3 of the 09/908,950 application are identical to claims 3 and 5 of the instant application. Independent claim 19 of the 09/908,950 application is a re-stated version of claim 1. Claim 29 is drawn to a method of claim 27 where the probes comprise cDNA and the first temperature is between 45 and 65 C, claim 30 is drawn to the first temperature being between 60 and 65 C, and claim 32 is drawn to the second temperature being from 45 to 55 C. Therefore, claims 1-3 of the 09/908,950 application anticipate claims 1, 3 and 5 of the instant application by having a target being RNA and the hybridization being performed at two different temperatures. Claim 19 of the 09/908,950 application anticipates claim 1 of the instant application, and claims 20 and 21 of the 09/908,950 application are identical to claims 3 and 5 of the instant application. Claims 30 and 32 anticipate claims 6-8 in that they are drawn to the first temperature being higher than the second temperature.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

14. Claims 1 and 3-5 are provisionally rejected on the ground of nonstatutory obviousness-type double patenting as being unpatentable over claims 23 and 30 of copending Application No. 10/234,069. Although the conflicting claims are not identical, they are not patentably distinct from

each other because claims 23 and 30 of the 10/234,069 application are species of claims 1, 3 and 5 of the instant application.

Specifically, claim 1 of the instant application is drawn to a method for determining the presence of at least one specific nucleotide sequence in a target nucleic acid reagent extracted from a biological sample, said method comprising the steps of:

(a) concurrently contacting a microarray with:

(i) a target nucleic acid reagent, said target nucleic acid reagent having a nucleotide sequence, said nucleotide sequence further including a capture sequence, and

(ii) a capture reagent, said capture reagent having at least one first arm having a label capable of emitting a detectable signal and at least one second arm having a nucleotide sequence complementary to said capture sequence of said target nucleic acid reagent;

said microarray having thereon a plurality of features, each of said plurality of features including a probe nucleotide sequence; and

(b) treating the microarray from step (a) at a temperature and for a time sufficient to induce said nucleotide sequence of said target nucleic acid to hybridize to the probe nucleotide sequence complementary thereto on the microarray, and to induce said capture reagent to hybridize to said capture sequence of said nucleotide sequence of said target nucleic acid hybridized to the microarray.

Claim 23 of the 10/234,069 application is drawn to a method, said method comprising the steps of:

1) using a microarray comprising a plurality of features, said features comprising a first set of nucleotide sequences;

2) contacting said microarray with a mixture comprising:

a) a first component comprising a cDNA reagent obtained from mRNA of a target sample, said cDNA having a capture sequence;

b) a second component comprising a dendrimer having at least one first arm comprising a label for producing a detectable signal and at least one second arm having a second nucleotide sequence complementary to said capture sequence; and,

c) a third component comprising a synthetic DNA oligonucleotide for use as a blocking reagent to reduce non-specific binding between said first set of nucleotide sequences and said first component, said synthetic DNA oligonucleotide comprising at least one nucleotide of LNA and consisting essentially of nucleotides used to compete with poly-A to poly-T hybridization between said first set of nucleotide sequences and said first component, further comprising the step of mixing said first component and said second component at a temperature and for a time sufficient to enable said first component to bind to the second component.

Claim 30 of the 10/234,069 application is drawn to a method for detection and assay on a microarray, said method comprising the steps of:

1) incubating a mixture including:

a) a first component comprising a cDNA reagent obtained from mRNA of a target sample, said cDNA having a capture sequence; and

b) a second component comprising a dendrimer having at least one first arm comprising a label for producing a detectable signal and at least one second arm having a second nucleotide sequence complementary to the capture sequence,

said mixture being incubated at a first temperature and for a time sufficient to induce the first component to bind to the second component and form a prehybridized cDNA-dendrimer complex;

2) contacting a microarray with said mixture, wherein said microarray comprises a plurality of features, said features comprising a first set of nucleotide sequences and wherein a third component comprising an synthetic DNA oligonucleotide comprising at least 20 normal nucleotides and at least two nucleotides of LNA is used as a blocking reagent to reduce non-specific binding between said first set of nucleotide sequences and said first component, by competing with poly-A to poly-T hybridization between said first set of nucleotide sequences and said first component; and,

3) incubating said microarray and said prehybridized cDNA-dendrimer complex at a second temperature and for a time sufficient to induce said prehybridized cDNA-dendrimer complex to bind any of said set of first nucleotide sequences that are complementary to any sequences of said cDNA reagent, wherein such binding results in said feature emitting said detectable signal such that a hybridization pattern is generated on said microarray.

Therefore, claim 23 anticipates claims 1, 3 and 5 since it is drawn to a method where a third component with blocking functionality is used. Claim 30 anticipates claims 1 and 3-5, since it is drawn to a method where the target is cDNA and there is an additional third component in the reaction mixture.

This is a provisional obviousness-type double patenting rejection because the conflicting claims have not in fact been patented.

15. No claims are allowed.

Conclusion

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Teresa E. Strzelecka whose telephone number is (571) 272-0789. The examiner can normally be reached on M-F (8:30-5:30).

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on (571) 272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Teresa E Strzelecka
Primary Examiner
Art Unit 1637

Teresa Strzelecka
12/7/06

Notice to Comply	Application No.	Applicant(s)	
	10/825,776	GETTS ET AL.	
	Examiner	Art Unit	
	Teresa E. Strzelecka	1637	

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to the final rulemaking notice published at 55 FR 18230 (May 1, 1990), and 1114 OG 29 (May 15, 1990). If the effective filing date is on or after July 1, 1998, see the final rulemaking notice published at 63 FR 29620 (June 1, 1998) and 1211 OG 82 (June 23, 1998).

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☒ 7. Other: Sequences on pages 47, 48 and 50 do not have accompanying SEQ ID NOs.

Applicant Must Provide:

☐ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☐ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
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